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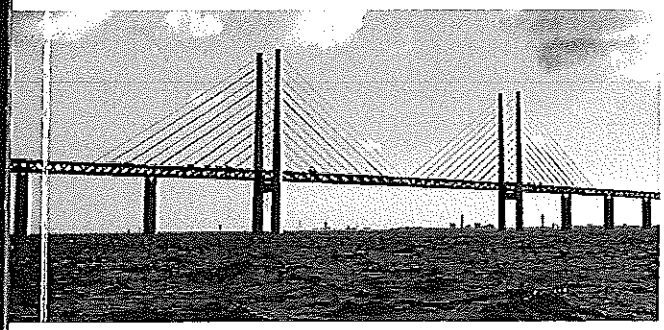

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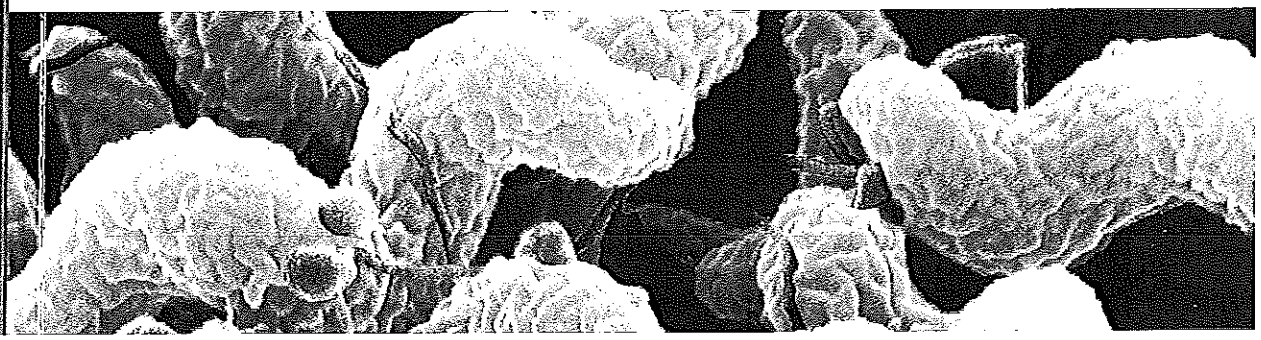

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PEA1.37 Microbiological study of *Nunu*, a spontaneously fermented milk of Ghana

Fortune Akabanda (1), K Tano-Debrah (2), R Glover (1), J Owusu-Kwarteng (1), D S. Nielsen (3), L Jespersen (3)
(1) University for Development Studies, Navrongo, Ghana
(2) University of Ghana, Legon, Ghana
(3) University of Copenhagen, Faculty of Life Science, Denmark

The nature of traditional African spontaneously fermented products varies from one region to another depending on the local indigenous microflora, which reflects the climatic conditions of the area, the raw materials used, the processing conditions etc. *Nunu* is a spontaneously fermented sour milk product used as a staple food amongst certain tribes of the West African Sub-Region. The production of *nunu* is more of an art than based on scientific description and so little or no scientific information exists on it. The main purpose of this study was to isolate, identify and characterize the microorganisms present in *nunu*. In this study a survey on the production of *nunu* in northern Ghana was carried out. The survey revealed that processing of *nunu* in northern Ghana takes place at ambient conditions in local containers called calabashes or plastic containers. No starter culture is added but the milk gets contaminated with microorganisms from the environment, processing equipments, or processors. Samples of *nunu* were collected from producers in three towns. The fermentation was followed from 0 to 24 hours with two hours interval. pH was followed during processing and *nunu* was at the end of the fermentation found to have a pH of 3.4. Microbial counts were determined on selective media and counts range from 4.00 to 9.00 log CFU/ml. A total of 198 microorganisms associated with the production were isolated. The microbial diversity was evaluated using Rep-PCR and agarose gel electrophoresis. This was followed by sequencing of the 16S rRNA gene. The predominant lactic acid bacteria in *nunu* include: *Lactobacillus fermentum, Lactobacillus plantarum, Lactobacillus helveticus, Lactobacillus delbrueckii, Leuconostoc mesenteriodes, Lactococcus garvieae, Enterococcus faecium, Enterococcus italicus, Weissella cibaria* and *Weissella confusa*. The results of the study do reveal that a great biodiversity of microorganisms are involved in *nunu* production and emphasize the need for selection and use of starter cultures in order to obtained controlled fermentations.

PEA1.38 Fermentation of Cassava fish (*Pseudotolithus sp.*)for new type of Ianhouin production by starter cultures of bacillus

Victor Bienvenu Anihouvi (1), E Sakyi-Dawson (2), GS Ayernor (3), J Houngouigan (4)
(1) University of Abomey-Calavi, Benin
(2) University of Ghana, Legon Accra, Ghana
(3) University of Ghana, Legon Accra, Ghana
(4) University of Abomey-Calavi, Benin

Two predominant strains of *Bacillus* species previously isolated during the spontaneous fermentation of *Ianhouin* were tested singly and in combination for their ability to ferment sterile flesh of cassava fish. The total viable cells pattern was enumerated according to Stevenson *et al.* (1992). The chemical changes occurring during the fermentation and the role of individual micro-organism were investigated according to Pearson's and AOAC methods. Gas Chromatography/Mass Spectrometry (GC-MS) system was used to detect aroma compounds in extracts of the inoculated fermenting samples. For all fermentations, a gradual increase in total viable cells was observed with final counts of 4.8×10^6, 1.6×10^6 and 3.7×10^6 cfu/g after 48 h of fermentation for *Bacillus subtilis, Bacillus licheniformis* and a mixed culture of *B. subtilis* and *B. licheniformis* respectively. The pH values as well as the proteolytic activities in the fermenting samples increased as the fermentation progressed. The histamine contents in all inoculated samples were very low and less than 1mg/100g sample. A total of 41 aroma compounds were detected in the inoculated samples with carbonyls and lipid-derived compounds as the predominant ones. These compounds consisted of 5 aliphatic hydrocarbons, 4 aromatic hydrocarbons, 5 esters, 6 ketones, 4 acids, 4 alcohols, 8 amines, 3 aldehydes and 1 amide. In contrast to the spontaneous fermentation, aroma compounds such as furan, phenol, thiazoles and pyrroles were not detected during the inoculated fermentation samples.

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ing of 33 morphotypes were
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species *Lactobacillus* sp (13
(10.63%), and *Lactobacillus*
largest number of isolates a
the presence of lactic acid
DGGE analysis were perform
dominance of *Lactobacillus*
not modified significantly. T
dependent method.

PEA1.40 Genotypic anc

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(1) University c
(2) Chr. Hanser

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